Reconstruction of a genome-scale metabolic model for the riboflavin producer fungus *Ashbya gossypii*

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Metabolic models are an important tool for *in silico* simulation of cells' behavior. Until now, a considerable number of metabolic models have been released for a wide range of microorganisms.
Ashbya gossypii is an industrial-relevant fungus intensively used for riboflavin production with no model reported until now. Despite its high similarity with *Saccharomyces cerevisiae* genome, *A. gossypii* contains only 4726 protein-coding genes and, contrarily to *S. cerevisiae,* has a filamentous growth. Here, we describe the first genome-scale metabolic reconstruction for *Ashbya gossypii*.
Initially the whole genome was functionally re-annotated and each metabolic gene was assigned to an EC number using several databases such as UniProt, SGD, AGD, ExPASy and BRENDA. A total of 1429 genes were assigned to the different enzymatic families: 35.4 % hydrolases; 35.8 % transferases; 28.8 % other enzymatic families. Of the 1429 genes, 59 were assigned to multiple EC numbers and among these 36 % had EC numbers from different enzymatic families.
The next step of the reconstruction was the elaboration of the reactions set. Re-annotation data was crossed with the curated models iMM904 and iIN800 from *S. cerevisiae*. Some databases like BRENDA, KEGG or Metacyc were used in the cases where data were not available and an in-house tool was used to predict the transport reactions from *A. gossypii* genome sequences. At the end of this step, a set with 1755 reactions and 926 metabolites was obtained.
Using the obtained set of reactions the metabolic network was analyzed for possible gaps. All the gaps were filled by adding specific reactions leading to a model able to predict cell growth.
Current efforts aim model's validation against experimental data in order to allow more accurate predictions of cell's phenotype. More specifically, it is expected a final model able to provide valuable genetic strategies that could lead to significant improvements on *A. gossypii* as a cell factory.